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 START 2521000 2
 GTTGGTCTCCTGCGGTGCCCGGAATCCAGTCAGAAGTTCCAGCCTGCCACTGTTCTCTGATGCCATG CCA GCA 3
 9
 START 2521000 3
 P T Q L F F P L I R N C E L S R I Y G T 23
 CCA ACT CAA CTG TTT TTT CCT CTC ATC CGT AAC TGT GAA CTG AGC AGG ATC TAT GGC ACT 69
 A C Y C H H K H L C C S S S Y I P Q S R 43
 GCA TGT TAC TGC CAC CAC AAA CAT CTC TGT TGT TCC TCA TCG TAC ATT CCT CAG AGT CGA 129
 L R Y T P H P A Y A T F C R P K E N W W 63
 CTG AGA TAC ACA CCT CAT CCA GCA TAT GCT ACC TTT TGC AGG CCA AAG GAG AAC TGG TGG 189
 Q Y T Q G R R Y A S T P Q K F Y L T P P 83
 CAG TAC ACC CAA GGA AGG AGA TAT GCT TCC ACA CCA CAG AAA TTT TAC CTC ACA CCT CCA 249
 Q V N S I L K A N E Y S F K V P E F D G 103
 CAA GTC AAT AGC ATC CTT AAA GCT AAT GAA TAC AGT TTC AAA GTG CCA GAA TTT GAC GGC 309
 K N V S S I L G F D S N Q L P A N A P I 123
 AAA AAT GTC AGT TCT ATC CTT GGA TTT GAC AGC AAT CAG CTG CCT GCA AAT GCA CCC ATT 369
 E D R R S A A T C L Q T R G M L L G V F 143
 GAG GAC CGG AGA AGT GCA GCA ACC TGC TTG CAG ACC AGA GGG ATG CTT TTG GGG GTT TTT 429
 D G H A G C A C S Q A V S E R L F Y Y I 163
 GAT GGC CAT GCA GGT TGT GCT TGT TCC CAG GCA GTC AGT GAA AGA CTC TTT TAT TAT ATT 489
 A V S L L P H E T L L E I E N A V E S G 183
 GCT GTC TCT TTG TTA CCC CAT GAG ACT TTG CTA GAG ATT GAA AAT GCA GTG GAG AGC GGC 549
 R A L L P I L Q W H K H P N D Y F S K E 203
 CGG GCA CTG CTA CCC ATT CTC CAG TGG CAC AAG CAC CCC AAT GAT TAC TTT AGT AAG GAG 609
 A S K L Y F N S L R T Y W Q E L I D L N 223
 GCA TCC AAA TTG TAC TTT AAC AGC TTG AGG ACT TAC TGG CAA GAG CTT ATA GAC CTC AAC 669
 T G E S T D I D V K E A L I N A F K R L 243
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 D N D I S L E A Q V G D P N S F L N Y L 263
 GAT AAT GAC ATC TCC TTG GAG GCG CAA GTT GGT GAT CCT AAT TCT TTT CTC AAC TAC CTG 789
 V L R V A F S G A T A C V A H V D G V D 283
 GTG CTT CGA GTG GCA TTT TCT GGA GCC ACT GCT TGT GTG GCC CAT GTG GAT GGT GTT GAC 849
 L H V A N T G D S R A M L G V Q E E D G 303
 CTT CAT GTG GCC AAT ACT GGC GAT AGC AGA GCC ATG CTG GGT GTG CAG GAA GAG GAC GGC 909

Figure 1A

S W S A V T L S N D H N A Q N E R E L E	323
TCA TGG TCA GCA GTC ACG CTG TCT AAT GAC CAC AAT GCT CAA AAT GAA AGA GAA CTA GAA	969
R L K L E H P K S E A K S V V K Q D R L	343
CGG CTG AAA TTG GAA CAT CCA AAG AGT GAG GCC AAG AGT GTC GTG AAA CAG GAT CGG CTG	1029
L G L L M P F R A F G D V K F K W S I D	363
CTT GGC TTG CTG ATG CCA TTT AGG GCA TTT GGA GAT GTA AAG TTC AAA TGG AGC ATT GAC	1089
L Q K R V I E S G P D Q L N D N E Y T K	383
CTT CAA AAG AGA GTG ATA GAA TCT GGC CCA GAC CAG TTG AAT GAC AAT GAA TAT ACC AAG	1149
F I P P N Y H T P P Y L T A E P E V T Y	403
TTT ATT CCT CCT AAT TAT CAC ACA CCT CCT TAT CTC ACT GCT GAG CCA GAG GTA ACT TAC	1209
H R L R P Q D K F L V L A T D G L W E T	423
CAC CGA TTA AGG CCA CAG GAT AAG TTT CTG GTG TTG GCT ACT GAT GGG TTG TGG GAG ACT	1269
M H R Q D V V R I V G E Y L T G M H H Q	443
ATG CAT AGG CAG GAT GTG GTT AGG ATT GTG GGT GAG TAC CTA ACT GGC ATG CAT CAC CAA	1329
Q P I A V G G Y K V T L G Q M H G L L T	463
CAG CCA ATA GCT GTT GGT GGC TAC AAG GTG ACT CTG GGA CAG ATG CAT GGC CTT TTA ACA	1389
E R R T K M S S V F E D Q N A A T H L I	483
GAA AGG AGA ACC AAA ATG TCC TCG GTA TTT GAG GAT CAG AAC GCA GCA ACC CAT CTC ATT	1449
R H A V G N N E F G T V D H E R L S K M	503
CGC CAC GCT GTG GGC AAC AAC GAG TTT GGG ACT GTT GAT CAT GAG CGC CTC TCT AAA ATG	1509
L S L P E E L A R M Y R D D I T I I V V	523
CTT AGT CTT CCT GAA GAG CTT GCT CGA ATG TAC AGA GAT GAC ATT ACA ATC ATT GTA GTT	1569
Q F N S H V V G A Y Q N Q	538
CAG TTC AAT TCT CAT GTT GTA GGG GCG TAT CAA AAC CAA GAA TAG	1614

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End of seq IDNO: 2
 End of seq IDNO: 3
 End of seq IDNO: 1

Figure 1.B

Analysis of 26583 (537 aa)

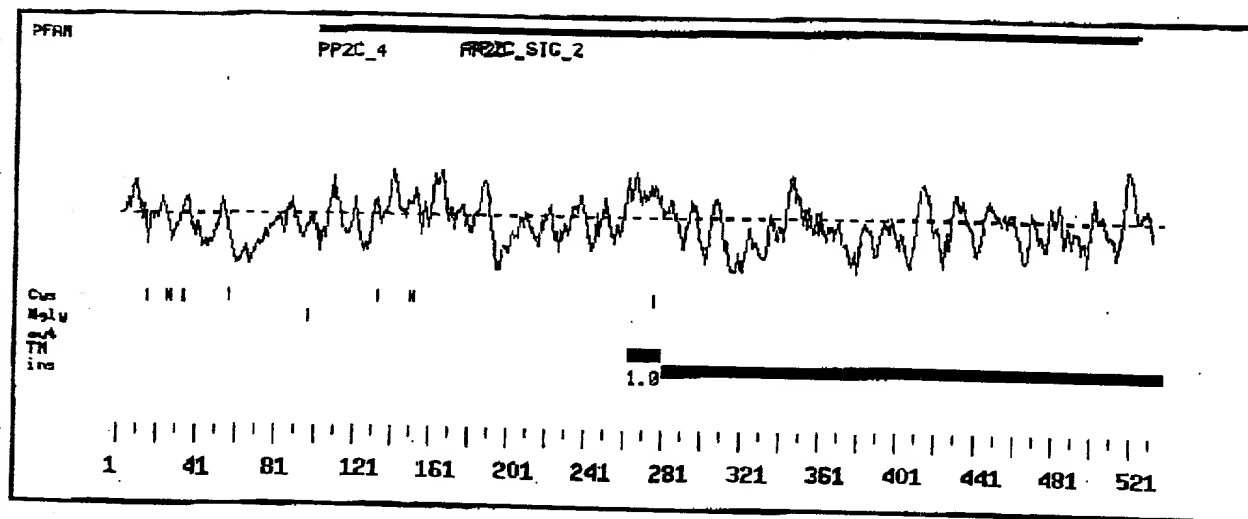


Figure 2

PP2C: domain 1 of 1, from 173 to 461: score 261.3, E = 1.3e-74

```

26583 173 -->ldvgvzmgwksmeDahialkninsasgkdsaffavfDGhgGs 218 SEQ ID NO:4
      1 ++++ + f +++ +++++ ++ s++ s+ +f +++ +
      LLEIENAVESGRALLPILQWHKHPNDYF-SKEASKLYFNSLRTYWQE 218 SEQ ID NO:2

      qaakyagkhkhk.tilaerksfpegdpwEmklsdledalkesfleadtde
      + *g++ +++ + a++ f+ +d+ d + +++++ +++++
26583 219 LIDLNTGESTDIDVKEALINAFKRLDN-----DISLEAQVGDPSFLNY 262

      elrsaeasaankvltkedlssGstAvvalirgnklyVANvGDSRavLern
      +++ + SG+TA+va+++g +L+VAN+GDSRa+L+ +
26583 263 LVLr-----VAFSGATACVAHVdGVdLHVANTGDSRAHLGVQ 299

      gnaikw.avtLteDHkPsnedErerIeaaGGfvarvs...ngRvnGVlav
      +++++w+avtL+DH+++ne+E+eR++ +++++ + +s +++R++G L++
26583 300 EEDGSW$AVTLSNDHNAQNERELERLKLHHPKSEAKSvvkQDRLLGLLMP 349

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26583 350 FRAFGDVKFKWSIDLQKRVIesGpDQlNDnEXTKfIPPhyhtpPYLTAEP 399

      dvtssstdltpdkDeFlilAcDGLWDvvsdqewvdivrselsdgnksaedp
      +vt +++l+p+ D+Fl+LA+DGLW++++ q+vv iv + l+ +
26583 400 EVT-YHRLRPQ-DKFLVLATDGLWETHRQDVVRIVGEYLTGM-----H 461

      maaaeklvdaaiargseDni<+
      ++ ++ + + g ++
26583 442 HQQPIAVGGYKVTLCQMHGL 461

```

Figure 3A

00001257-030604

PF2C_4: domain 1 of 1, from 99 to 523; score 138.5, E = 7.6e-98

```

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26583 145 GHACCACSOAVSERLFYYIAVSLPHETLLEIENAVEsGRaLlPflqwhk 194
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+++ ++ ++ ++ +++++ +ln+g+++ dv+aal++aF+r+d
26583 195 hndyfskeasklyfnslrtywqelidlnEGESTDIDVKEALINAFKRLD 244
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++i+ + + +++++ + + + +TA+va++g +l+vAN+GDSRa
26583 245 NDIslaeaqvgdpsflnylvrvaFsgATACVAHVdGVdLHVANTGDSRa 294
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+L+ + +d+sw sav L+DH++ ne+E+aR++ +++++ a +++
26583 295 MLGVQEEDqSW-----SAVTLSDHNAQNERELERLKLHMPKSE--AKS 336
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26583 337 VVKQD-----RLGL---LMPFRAFgDVKFKwsIDLqKrVIEsgpdqLNd 378
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26583 379 NEYTKFIPPNYHTPPYLTAEPVTYHRL-----RPQDKFLVLATDGLWE 422
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26583 423 TMRQDVVRIVGEYLTGHHQQLAVGCKVTlGmHClteRrtkmsav 472
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++++ ++l R+ +++++ ++L +++ ++ + +D+it++v
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                                     v+-
                                     v
26583 523 V 523

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SEQ ID NO:5

SEQ ID NO:2

Figure 3B

